FIGURE   S1   **Motif   'NPAVLRKLCIEAKISNTTTDSRCPTQGEATLVEEQDANFVCRRTFVDRGW'**

containing the epitope 'RCPTQGE' as 100% conserved region in all sequences of envelope protein.

FIGURE S2 (A) **Linear B-cell epitope prediction, (B) Antigenicity prediction, (C) Surface accessibility prediction, (D) Hydrophilicity prediction, (E) flexibility prediction graphs of epitope 'RCPTQGE' of envelope protein.** The graphs were plotted between the score for predicted epitope and the position of epitope in protein sequence. The red line represents the threshold value used for epitope prediction. The yellow region indicates the possible region of B-cell epitope in the protein sequence.
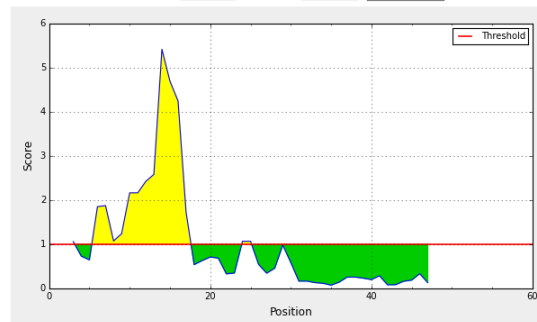

a)

b)
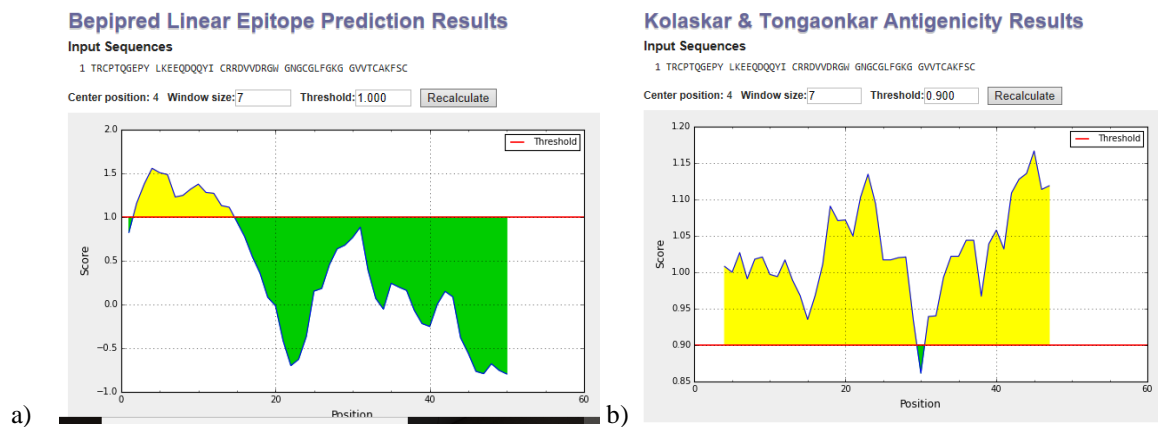
Emini Surface Accessibility Prediction Results

Input Sequences

1 TRCPTQGEPY LKEEQDQQYI CRRDVVDRGW GNGCGLFGKG GVVTCAKFSC

Center position: 3 Window size: 6   Threshold: 1.000   Recalculate
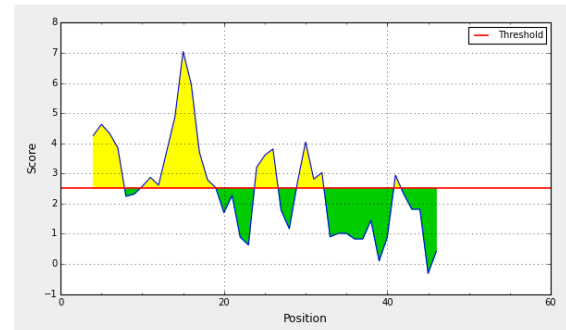
c)

Parker Hydrophilicity Prediction Results

Input Sequences

1 TRCPTQGEPY LKEEQDQQYI CRRDVVDRGW GNGCGLFGKG GVVTCAKFC

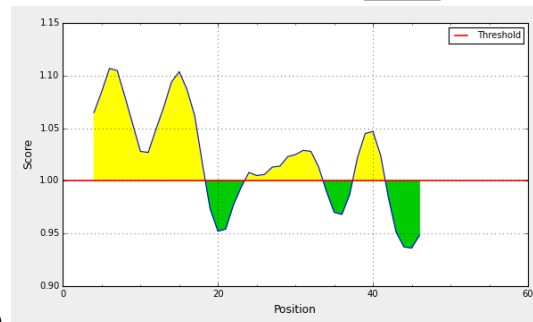Center position: 4 Window size: 7   Threshold: 2.511   Recalculate

d)

Karplus & Schulz Flexibility Prediction Results

Input Sequences

1 TRCPTQGEPY LKEEQDQQYI CRRDVVDRGW GNGCGLFGKG GVVTCAKFSC

Center position: 4 Window size: 7   Threshold: 1.000   Recalculate

e)

FIGURE S3 Three- dimensional visualization of predicted epitope 'RCPTQGE' of envelope protein. Predicted epitope was mapped on CryoEM structure of Dengue virus envelope protein heterotetramer (pdb id 3J2P) using CHIMERA visualization tool.

FIGURE S4 **Motif 'SAAQRRGRIGRNQNKEGDY' containing the epitope 'SAAQRRGR' as 100% conserved region in all sequences of protein NS3.**

FIGURE S5 (A) **Linear B-cell epitope prediction, (B) Antigenicity prediction, (C) Surface accessibility prediction, (D) Hydrophilicity prediction, (E) flexibility prediction graphs of epitope 'SAAQRRGR' of NS3.** The graphs were plotted between the score for predicted epitope and the position of epitope in protein sequence. The red line represents the threshold value used for epitope prediction. The yellow region indicates the possible region of B-cell epitope in the protein sequence.

Bepipred Linear Epitope Prediction Results

Input Sequences
1 PRRCLKPVIL KGPERVILAG PMPVTVASAA QRRGRIGRNQ NKEGD

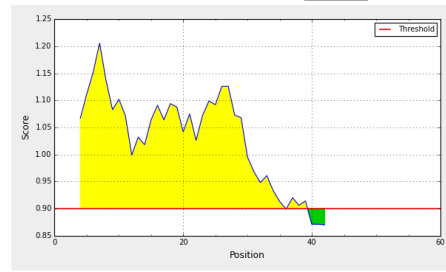Center position: 4 Window size: 7 Threshold: 1.000 Recalculate

a)

Kolaskar & Tongaonkar Antigenicity Results

Input Sequences
1 PRRCLKPVIL KGPERVILAG PMPVTVASAA QRRGRIGRNQ NKEGD

Center position: 4 Window size: 7 Threshold: 0.900 Recalculate
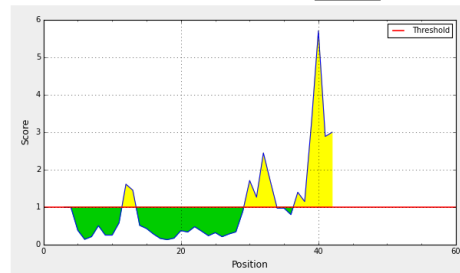
b)

Emini Surface Accessibility Prediction Results

Input Sequences
1 PRRCLKPVIL KGPERVILAG PMPVTVASAA QRRGRIGRNQ NKEGD

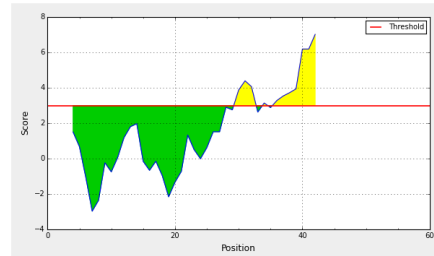Center position: 3 Window size: 6 Threshold: 1.000 Recalculate

c)

Parker Hydrophilicity Prediction Results

Input Sequences
1 PRRCLKPVIL KGPERVILAG PMPVTVASAA QRRGRIGRNQ NKEGD

Center position: 4 Window size: 7 Threshold: 3.000 Recalculate
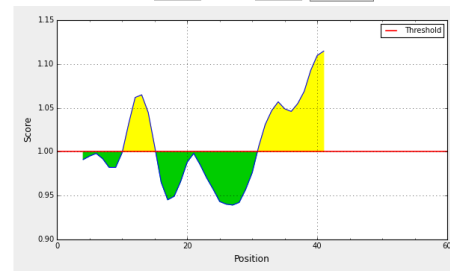
d)

Karplus & Schulz Flexibility Prediction Results

Input Sequences
1 PRRCLKPVIL KGPERVILAG PMPVTVASAA QRRGRIGRNQ NKEGD

Center position: 4 Window size: 7 Threshold: 1.000 Recalculate
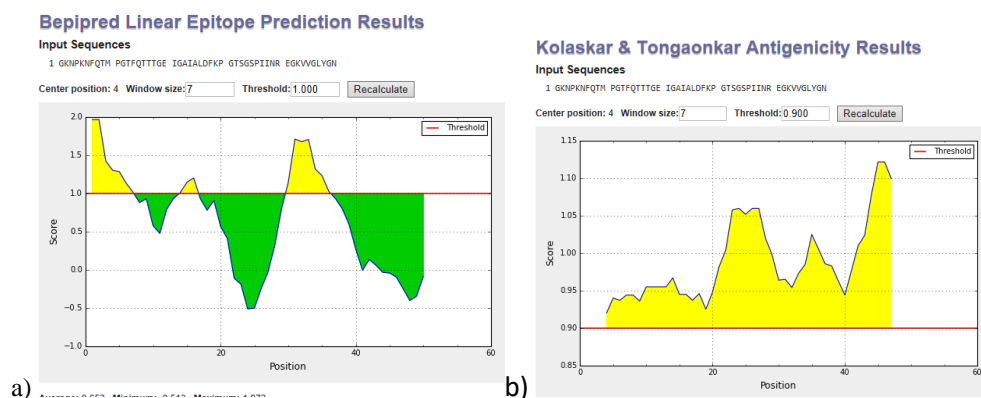
e)

FIGURE S6 Three- dimensional visualization of predicted epitope 'SAAQRRGR' of NS3 protein. The 3D structure of protein was predicted using I-TASSER server and the predicted epitope were localized in these 3-D structure and visualized using CHIMERA visualization tool.

FIGURE S7 **Motif 'GKNPKNFQTMPGTFQTTTGEIGAIALDFKPGTSGSPIINR EGKVVGLYGN' containing the epitope 'PGTSGSPI' as 100% conserved region in all sequences of NS3 protein.**

FIGURE S8 (A) **Linear B-cell epitope prediction, (B) Antigenicity prediction, (C) Surface accessibility prediction, (D) Hydrophilicity prediction, (E) flexibility prediction graphs of epitope 'PGTSGSPI' of NS3.** The graphs were plotted between the score for predicted epitope and the position of epitope in protein sequence. The red line represents the threshold value used for epitope prediction. The yellow region indicates the possible region of B-cell epitope in the protein sequence.
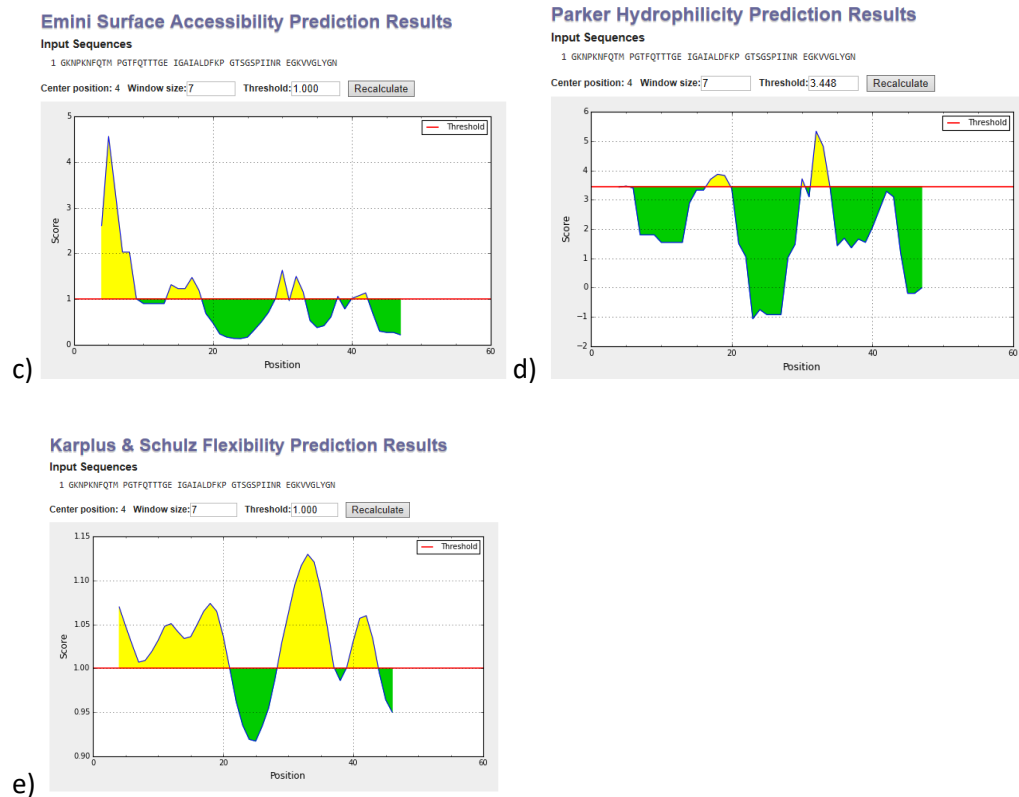

a)

b)

Emini Surface Accessibility Prediction Results
Input Sequences
1 GKNPKNFQTM PGTFQTTTGE IGAIALDFKP GTSGSPIINR EGKVVGLYGN

Center position: 4 Window size: 7 Threshold: 1.000 Recalculate

c)

Parker Hydrophilicity Prediction Results
Input Sequences
1 GKNPKNFQTM PGTFQTTTGE IGAIALDFKP GTSGSPIINR EGKVVGLYGN

Center position: 4 Window size: 7 Threshold: 3.448 Recalculate

d)

Karplus & Schulz Flexibility Prediction Results
Input Sequences
1 GKNPKNFQTM PGTFQTTTGE IGAIALDFKP GTSGSPIINR EGKVVGLYGN

Center position: 4 Window size: 7 Threshold: 1.000 Recalculate

e)

FIGURE S9 Three- dimensional visualization of predicted epitope 'PGTSGSPI' of NS3 protein. The predicted epitope were localized in the 3-D structure of DENV protein NS3 (pdb id 2FOM) and visualized using CHIMERA visualization tool.

FIGURE S10 **Motif 'CVMASSVLLWMASVEPHWIAASIILEFFLMVLLIPEPDRQRTPQDNQLAY' containing the epitope 'QRTPQDNQL' as 100% conserved region in all sequences of NS4A protein.**

FIGURE S11 (A) **Linear B-cell epitope prediction, (B) Antigenicity prediction, (C) Surface accessibility prediction, (D) Hydrophilicity prediction, (E) flexibility prediction graphs of epitope 'QRTPQDNQL' of NS4A.** The graphs were plotted between the score for predicted epitope and the position of epitope in protein sequence. The red line represents the threshold value used for epitope prediction. The yellow region indicates the possible region of B-cell epitope in the protein sequence.
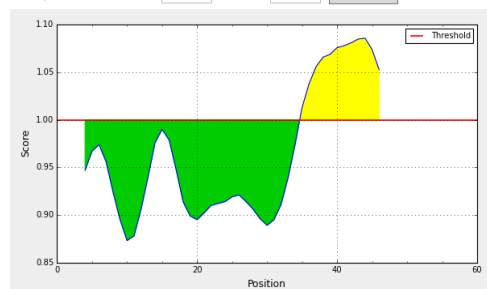

a)

b)

c)

d)
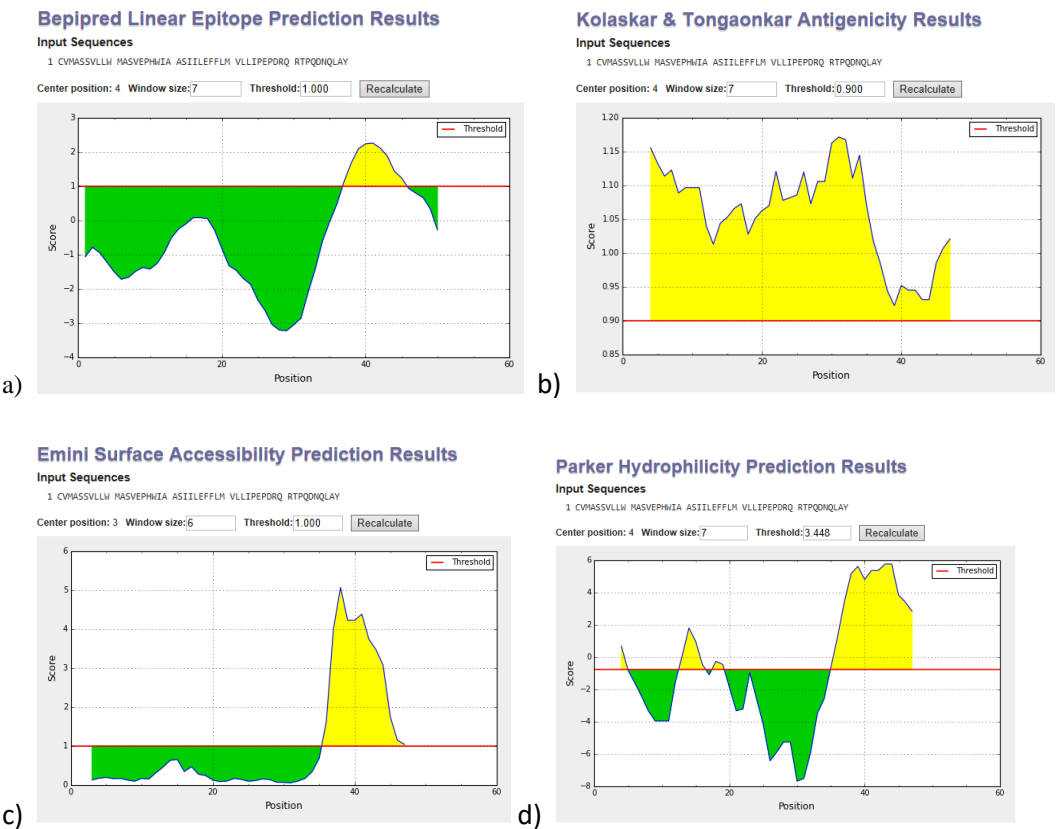
Karplus & Schulz Flexibility Prediction Results

Input Sequences

1 CVMASSVLLW MASVEPHWIA ASIILEFFLM VLLIPEPDRQ RTPQDNQLAY

Center position: 4 Window size: 7 Threshold: 1.000 Recalculate

e)

FIGURE S12 Three- dimensional visualization of predicted epitope 'QRTPQDNQL' of NS4A protein. The 3D structure of protein was predicted using I-TASSER server and the predicted epitope were localized in these 3-D structure and visualized using CHIMERA visualization tool.
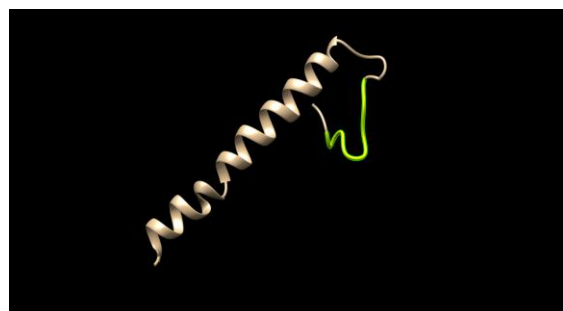

FIGURE S13 **Motif 'HYAIIGPGLQAKATREAQKRAAAGIM' containing the epitope 'LQAKATREAQKRA' as 100% conserved region in all sequences of NS4B protein.**

FIGURE S14 (A) **Linear B-cell epitope prediction, (B) Antigenicity prediction, (C) Surface accessibility prediction, (D) Hydrophilicity prediction, (E) flexibility prediction graphs of epitope 'LQAKATREAQKRA' of NS4B.** The graphs were plotted between the score for predicted epitope and the position of epitope in protein

sequence. The red line represents the threshold value used for epitope prediction. The yellow region indicates the possible region of B-cell epitope in the protein sequence.
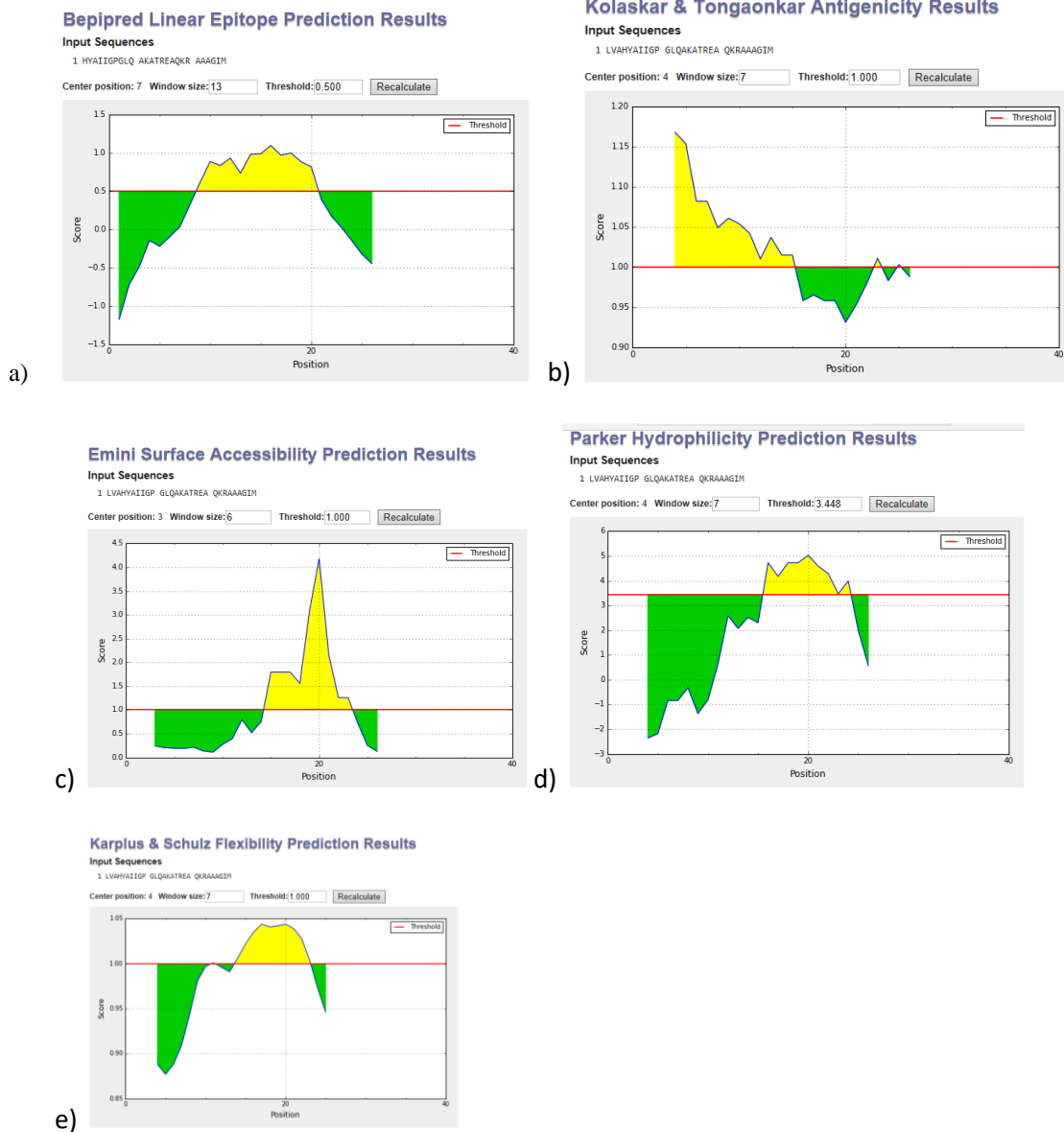

a)

b)

c)

d)

e)

FIGURE S15 Three- dimensional visualization of predicted epitope 'LQAKATREAQKRA' of NS4B. The 3D structure of protein was predicted using I-TASSER server and the predicted epitope were localized in these 3-D structure and visualized using CHIMERA visualization tool.